

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:39:01 ; Search time 585.791 Seconds
(without alignments)
11011.138 Million cell updates/sec

Title: US-09-856-681A-3

Perfect score: 216

Sequence: 1 ccgcccggccggcccgagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gssl:
 29: gb_gss2:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query	%	No.	Score	Match	Length	DB	ID	Description
				1	216	100.0	495	12	BM855120	BM855120 K-EST0137
				2	216	100.0	496	9	AV704776	AV704776 AV704776
				3	216	100.0	815	13	BU850016	BU850016 AGENCOURT
				4	216	100.0	862	13	BQ723018	BQ723018 AGENCOURT
				5	216	100.0	928	10	BE898612	BE898612 601681550
				6	216	100.0	1013	10	BE899378	BE899378 601681309
				7	215	99.5	494	14	N31401	N31401 yx67d08.rl
				8	212.8	98.5	6875	11	BC032619	BC032619 Homo sapi
				9	212	98.1	462	14	N25829	N25829 yx22d01.rl
				10	203.6	94.3	410	14	N46020	N46020 yy35a05.rl
				11	193.6	89.6	632	14	CB577257	CB577257 AMGNNUC:C
				12	193.6	89.6	711	14	CB246380	CB246380 UI-M-FI0-
				13	193.6	89.6	2411	14	CB605722	CB605722 AMGNNUC:M
c	14	178	82.4		291	10	BF702343		BF702343 MI-P-A2-a	
	15	177.2	82.0		1183	12	BM546059		BM546059 AGENCOURT	
c	16	166.4	77.0		364	9	AA729933		AA729933 nx40f11.s	
	17	166.2	76.9		628	9	AA625166		AA625166 af67e09.r	
	18	161	74.5		304	9	AA369179		AA369179 EST80573	
	19	161	74.5		624	10	AW957071		AW957071 EST369141	
	20	159.6	73.9		486	10	BF775045		BF775045 285089 MA	
	21	159.6	73.9		598	9	AV593974		AV593974 AV593974	
c	22	154	71.3		556	9	AA909230		AA909230 ol12h08.s	
c	23	141.8	65.6		342	14	CB693654		CB693654 AMGNNUC:C	
	24	135.6	62.8		895	12	BI819955		BI819955 603035314	
	25	117.6	54.4		841	13	BU390763		BU390763 603511251	
	26	117.6	54.4		841	13	BU394026		BU394026 603802267	
c	27	110.6	51.2		1201	9	AL543312		AL543312 AL543312	
	28	104.8	48.5		581	14	CB426060		CB426060 601199 MA	
	29	104.8	48.5		852	10	BF306161		BF306161 601893009	
	30	102.6	47.5		732	13	BQ180391		BQ180391 UI-M-EX0-	
	31	99	45.8		543	12	BG698043		BG698043 602659189	
	32	91.8	42.5		773	14	CF290712		CF290712 AGENCOURT	
	33	90.2	41.8		566	12	BJ060286		BJ060286 BJ060286	
	34	89.4	41.4		409	14	W92871		W92871 zd92h03.rl	
c	35	84.6	39.2		602	14	N22686		N22686 yx64c02.s1	
	36	71.8	33.2		145	10	BG003350		BG003350 RC0-GN013	
	37	62.8	29.1		829	12	BI824613		BI824613 603033546	
	38	58.8	27.2		685	10	BE265000		BE265000 601193829	
c	39	58.4	27.0		589	14	CB426401		CB426401 601583 MA	
	40	56	25.9		350	14	CD804283		CD804283 UI-M-GV0-	
c	41	55	25.5		420	10	BE709445		BE709445 IL3-HT061	
	42	55	25.5		708	14	CD356790		CD356790 AGENCOURT	
	43	55	25.5		740	12	BG571342		BG571342 602592610	
	44	55	25.5		792	10	BE543221		BE543221 601069213	
	45	55	25.5		3405	11	BC004330		BC004330 Homo sapi	

ALIGNMENTS

RESULT 1
BM855120

LOCUS BM855120 495 bp mRNA linear EST 06-MAR-2002

DEFINITION K-EST0137909 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-150-D07
5', mRNA sequence.

ACCESSION BM855120

VERSION BM855120.1 GI:19211519

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 495)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 150 row: D column: 07
High quality sequence stop: 495.

FEATURES Location/Qualifiers

source 1. .495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-150-D07"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 100.0%; Score 216; DB 12; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.8e-44;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCGCCGCCGCAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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 Db 39 CCGCCGCCGCAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 98
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 Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 120
 |||||||
 Db 99 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 158
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 Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
 |||||||
 Db 159 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 218
 |||||||
 Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
 |||||||
 Db 219 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 254

RESULT 2

AV704776

LOCUS AV704776 496 bp mRNA linear EST 09-OCT-2000
 DEFINITION AV704776 ADB Homo sapiens cDNA clone ADBBJC04 5', mRNA sequence.
 ACCESSION AV704776
 VERSION AV704776.1 GI:10722088
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 496)
 AUTHORS Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G.,
 Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z.,
 Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S.,
 Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
 TITLE Homo sapiens cDNA ADB clones
 JOURNAL Unpublished (2000)
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 FEATURES Location/Qualifiers
 source 1..496
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ADBBJC04"
 /tissue_type="Adrenal gland"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="ADB"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.8e-44;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 181 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 240

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 241 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 300

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 301 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 360

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 361 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 396

RESULT 3

BU850016

LOCUS BU850016 815 bp mRNA linear EST 16-OCT-2002

DEFINITION AGENCOURT_10438272 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6598770 5', mRNA sequence.

ACCESSION BU850016

VERSION BU850016.1 GI:24034979

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 815)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2832 row: b column: 18
High quality sequence stop: 700.

FEATURES Location/Qualifiers

source 1. .815
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6598770"
/tissue_type="teratocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 815;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCAGGTGCACAGCTCCCAGCCATCTGGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 CCGCCGCCGCCGCAGAGGGTGGACTCCATCAGGTGCACAGCTCCCAGCCATCTGGC 155

Qy 61 CAGGCCGTACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 CAGGCCGTACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 215

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGACGTACCCCCCAAACCATCCTTGCTCCC 275

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 311

RESULT 4

BQ723018

LOCUS BQ723018 862 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8099701 Lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6190272 5', mRNA sequence.
ACCESSION BQ723018
VERSION BQ723018.1 GI:21861915
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM13588 row: n column: 01
High quality sequence stop: 592.

FEATURES Location/Qualifiers
source 1. .862
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6190272"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCG(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 862;
Best Local Similarity 100.0%; Pred. No. 3.6e-44;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 269 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 328

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 329 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 388

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 389 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 448

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 449 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 484

RESULT 5

BE898612

LOCUS BE898612 928 bp mRNA linear EST 29-SEP-2000

DEFINITION 601681550F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951685 5',
mRNA sequence.

ACCESSION BE898612

VERSION BE898612.1 GI:10365266

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 928)
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
CONTACT Contact: Robert Strausberg, Ph.D.
EMAIL Email: cgapbs-r@mail.nih.gov
TISSUE PROCUREMENT Tissue Procurement: DCTD/DTP
cDNA LIBRARY PREPARATION cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA LIBRARY ARRAYED BY cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA SEQUENCING BY DNA Sequencing by: Incyte Genomics, Inc.
CLONE DISTRIBUTION Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
PLATE LLCM820 row: c column: 14
HIGH QUALITY SEQUENCE STOP High quality sequence stop: 794.
FEATURES Location/Qualifiers
SOURCE 1. .928
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3951685"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_9"
 /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match	100.0%	Score	216	DB	10	Length	928
Best Local Similarity	100.0%	Pred. No.	3.7e-44				
Matches	216	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	CCGCCGCCGCCCGCAGAGGGTGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	60				
Db	243	CCGCCGCCGCCCGCAGAGGGTGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	302				
Qy	61	CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG	120				
Db	303	CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG	362				
Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC	180				
Db	363	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC	422				
Qy	181	CTTCCACATCCATGAAGCCCAATGATGCGTGTACA	216				
Db	423	CTTCCACATCCATGAAGCCCAATGATGCGTGTACA	458				

RESULT 6

BE899378

LOCUS BE899378 1013 bp mRNA linear EST 29-SEP-2000

DEFINITION 601681309F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951266 5', mRNA sequence.

ACCESSION BE899378

VERSION BE899378.1 GI:10367019

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1013)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM819 row: b column: 03
High quality sequence start: 30
High quality sequence stop: 828.

FEATURES Location/Qualifiers

source 1..1013
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3951266"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 216; DB 10; Length 1013;
Best Local Similarity 100.0%; Pred. No. 3.9e-44;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 CCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 351

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 411

Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC	180
Db	412	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC	471
Qy	181	CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA	216
Db	472	CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA	507

RESULT 7

N31401
 LOCUS N31401 494 bp mRNA linear EST 10-JAN-1996
 DEFINITION yx67d08.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone
 IMAGE:266799 5', mRNA sequence.
 ACCESSION N31401
 VERSION N31401.1 GI:1151800
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 494)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 464
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: T7
 High quality sequence stop: 464.
 FEATURES Location/Qualifiers
 source 1. .494
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3876441"
 /db_xref="taxon:9606"
 /clone="IMAGE:266799"
 /sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares melanocyte 2NbHM"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTT
 double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 99.5%; Score 215; DB 14; Length 494;
Best Local Similarity 99.5%; Pred. No. 5e-44;
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 60 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGNC 119

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 120 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 179

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 180 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 239

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 240 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 275

RESULT 8

BC032619

LOCUS BC032619 6875 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, similar to sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:5578066, mRNA.
ACCESSION BC032619
VERSION BC032619.1 GI:22749800
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6875)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nhgri.nih.gov
Akter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghghi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 69 Row: o Column: 4

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11991659

This clone has the following problem: retained intron.

FEATURES	Location/Qualifiers
source	1. .6875 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5578066" /tissue_type="Skin, melanotic melanoma." /clone_lib="NIH_MGC_72" /lab_host="DH10B" /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 98.5%; Score 212.8; DB 11; Length 6875;
Best Local Similarity 99.1%; Pred. No. 5.8e-43;
Matches 214; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db	3666 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCGGTGCACAGCTCCCAGCCATCTGGC 3725
Qy	61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 120
Db	3726 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 3785
Qy	121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db	3786 GGGCTGTAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3845
Qy	181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
Db	3846 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3881

RESULT 9

N25829

LOCUS N25829 462 bp mRNA linear EST 29-DEC-1995
DEFINITION yx22d01.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:262465 5', mRNA sequence.
ACCESSION N25829
VERSION N25829.1 GI:1140177
KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 462)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 360
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1117 Std Error: 0.00
 Seq primer: T7
 High quality sequence stop: 360.
 FEATURES Location/Qualifiers
 source 1. .462
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3872107"
 /db_xref="taxon:9606"
 /clone="IMAGE:262465"
 /sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares melanocyte 2NbHM"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo. RNA from normal foreskin melanocytes
 (FS374) was kindly provided by Dr. Anthony P. Albino."
 ORIGIN
 Query Match 98.1%; Score 212; DB 14; Length 462;
 Best Local Similarity 98.1%; Pred. No. 2.8e-43;
 Matches 212; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 238 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 297
 Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 120

Db	298	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGNCTACAANTCACTGACAAGGTTCG	357
Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC	180
Db	358	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCNTTGNTCCC	417
Qy	181	CTTTCCACATCCATGAAGCCAATGATGCGTGTACA	216
Db	418	CTTTCCACATCCATGAAGCCAATGATGCGTGTACA	453

RESULT 10

N46020

LOCUS N46020 410 bp mRNA linear EST 14-FEB-1996
 DEFINITION yy35a05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
 IMAGE:273200 5', mRNA sequence.
 ACCESSION N46020
 VERSION N46020.1 GI:1187186
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 410)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: T7
 High quality sequence stop: 329.
 FEATURES Location/Qualifiers
 source 1..410
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3882842"
 /db_xref="taxon:9606"
 /clone="IMAGE:273200"
 /sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares melanocyte 2NbHM"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 94.3%; Score 203.6; DB 14; Length 410;
Best Local Similarity 98.1%; Pred. No. 3.5e-41;
Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 CCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
|| ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 78 CCGCCCCACCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 137

Qy 67 GTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTGGGGCTG 126
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 138 GTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTGGGGCTG 197

Qy 127 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCTTC 186
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 198 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCTTC 257

Qy 187 ACATCCATGAAGCCAATGATGCGGTGTACA 216
|||||||||||||||||||||||||||||||
Db 258 ACATCCATGAAGCCAATGATGCGGTGTACA 287

RESULT 11

CB577257

LOCUS CB577257 632 bp mRNA linear EST 03-APR-2003
DEFINITION AMGNNUC:CDRG1-00015-G10-A cdrg1 (10898) *Rattus norvegicus* cDNA clone cdrg1-00015-g10 5', mRNA sequence.
ACCESSION CB577257
VERSION CB577257.1 GI:29521298
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00015 row: g column: 10.
FEATURES Location/Qualifiers
source 1. .632
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="cdrg1-00015-g10"

/tissue_type="Chung Model Ipsilate"
/clone_lib="cdrg1 (10898)"
/note="Vector: pSPORT1; Chung Model Rat DRG Left L5/L6"

ORIGIN

Query Match 89.6%; Score 193.6; DB 14; Length 632;
Best Local Similarity 93.5%; Pred. No. 1.5e-38;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|| ||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||
Db 20 CCACCTCCGCCCGCAGAGGGTGGACTCTATCCAGGTGCACAGCCCCAGCCCTCTGGC 79

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTG 120
||||||||||||| ||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||
Db 80 CAGGCCGTGACTGTTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACGAGGTG 139

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC 180
||||||||||| ||||||||||||||| ||||||||||||||| ||||||||||||||| |||||
Db 140 GGGCTGAAGCGCACCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTGCCCC 199

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
|||||||||||||||||||||||||||||||||
Db 200 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 235

RESULT 12

CB246380

LOCUS CB246380 711 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FI0-cdw-i-10-0-UI.r1 NIH_BMAP_FI0 Mus musculus cDNA clone
IMAGE:6835379 5', mRNA sequence.
ACCESSION CB246380
VERSION CB246380.1 GI:28368024
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 711)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 563-665, >(CA)n#Simple_repeat
Seq primer: pYX-5.

FEATURES Location/Qualifiers

source 1. .711
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6835379"
/tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F10"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 89.6%; Score 193.6; DB 14; Length 711;
Best Local Similarity 93.5%; Pred. No. 1.5e-38;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|| || ||||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 2 CCACCCCCCGCCCCGCAGCGGGTGGACTCTATCCAGGTGCACAGCTCCCAGCCCTCTGGC 61

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACACTCACTGACAAGGTGCG 120
|||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 62 CAGGCCGTGACTGTTCGAGGCAGCCCAGCCTCAATGCCTACAACACTCACTGACGAGGTGCG 121

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
|||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 122 GGGCTGAAGCGCACCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTGCTCCC 181

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
|||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 182 CTTTCCACATCCATGAAGCCAATGATGCATGTACA 217

RESULT 13

CB605722

LOCUS CB605722 2411 bp mRNA linear EST 16-MAY-2003
DEFINITION AMGNNUC:MRPE3-00075-D4-WY placenta embryo D17 (10379) Rattus
norvegicus cDNA clone mrpe3-00075-d4, mRNA sequence.
ACCESSION CB605722
VERSION CB605722.1 GI:29545334
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
REFERENCE 1 (bases 1 to 2411)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00075 row: d column: 4.
FEATURES Location/Qualifiers
 source 1. .2411
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="mrpe3-00075-d4"
 /tissue_type="placenta embryo"
 /clone_lib="placenta embryo D17 (10379)"
 /note="Vector: pSPORT1; placenta embryo D17"
ORIGIN
 Query Match 89.6%; Score 193.6; DB 14; Length 2411;
 Best Local Similarity 93.5%; Pred. No. 2.6e-38;
 Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 CCGCCGCCGCCGCCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
 || || ||||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1340 CCACCTCCGCCCGCAGAGGGTGGACTCTATCCAGGTGCACAGCCCCAGCCCTCTGGC 1399
 Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCTACAACACTCACTGACAAGGTG 120
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1400 CAGGCCGTGACTGTTCGAGGCAGCCCAGCCTAACGCTACAACACTCACTGACGAGGTG 1459
 Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1460 GGGCTGAAGCGCACCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTGCCCCC 1519
 Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 1520 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1555
RESULT 14
BF702343/c
LOCUS BF702343 291 bp mRNA linear EST 22-DEC-2000
DEFINITION MI-P-A2-aas-a-02-1-UM.s1 MI-P-A2 Sus scrofa cDNA clone
 MI-P-A2-aas-a-02-1-UM 3', mRNA sequence.
ACCESSION BF702343
VERSION BF702343.1 GI:11987751
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

Db 107 ACATCCATGAAGCCCATTGACGCGTGTACA 78
||||||||||||||||||||| |||||||||

RESULT 15

BM546059

LOCUS BM546059 1183 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6497880 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588479
5', mRNA sequence.
ACCESSION BM546059
VERSION BM546059.1 GI:18778712
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1183)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12359 row: k column: 08
High quality sequence stop: 725.
FEATURES Location/Qualifiers
source 1..1183
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/clone="IMAGE:5588479"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

ORIGIN

Query Match 82.0%; Score 177.2; DB 12; Length 1183;
Best Local Similarity 97.2%; Pred. No. 2.7e-34;
Matches 212; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
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Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTC- 119
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Qy 120 GGGGCTGAAGCGTACG-CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTC 178
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Db 861 GGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTC 920
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Db 921 CCCTTTCACATCCATGAAAGCCCCATGATGCGTGTAC 958

Search completed: March 26, 2004, 06:35:42

Job time : 590.791 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 21:56:51 ; Search time 858.974 Seconds
(without alignments)
10899.164 Million cell updates/sec

Title: US-09-856-681A-3

Perfect score: 216

Sequence: 1 ccggccgcccgcggcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	216	100.0	216	6	AX026743	AX026743 Sequence
2	216	100.0	2123	6	AX876167	AX876167 Sequence
3	216	100.0	2123	6	BD155987	BD155987 Primer fo
4	216	100.0	2123	9	AK027439	AK027439 Homo sapi
5	216	100.0	2227	6	BD127394	BD127394 Primer fo
6	216	100.0	2227	9	AK074975	AK074975 Homo sapi
7	216	100.0	2293	6	AX879422	AX879422 Sequence
8	216	100.0	2293	6	BD157826	BD157826 Primer fo
9	216	100.0	2293	9	AK027471	AK027471 Homo sapi
10	216	100.0	2306	6	AX882662	AX882662 Sequence
11	216	100.0	2306	6	BD159853	BD159853 Primer fo
12	216	100.0	2306	9	AK027654	AK027654 Homo sapi
13	216	100.0	3041	6	AX882248	AX882248 Sequence
14	216	100.0	3041	6	BD159617	BD159617 Primer fo
15	216	100.0	3041	9	AK027501	AK027501 Homo sapi
16	216	100.0	3093	6	AX026741	AX026741 Sequence
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18	216	100.0	3498	6	BD274938	BD274938 POLYNUCLE
19	216	100.0	3550	6	AX099520	AX099520 Sequence
20	216	100.0	3550	6	BD190797	BD190797 Secreted
21	216	100.0	3634	9	AK096337	AK096337 Homo sapi
22	216	100.0	3862	6	AX026746	AX026746 Sequence
23	216	100.0	3862	9	AF279656	AF279656 Homo sapi
24	216	100.0	4250	9	AB037789	AB037789 Homo sapi
25	216	100.0	4982	6	AX780545	AX780545 Sequence
26	216	100.0	6060	6	AX884099	AX884099 Sequence
27	216	100.0	6060	6	BD160721	BD160721 Primer fo
28	216	100.0	6060	9	AK027867	AK027867 Homo sapi
29	216	100.0	131823	2	AC010497	AC010497 Homo sapi
c 30	216	100.0	134349	9	AC010296	AC010296 Homo sapi
31	216	100.0	154061	9	AC008524	AC008524 Homo sapi
32	216	100.0	179647	2	AC108124	AC108124 Homo sapi
c 33	216	100.0	188207	2	AC010233	AC010233 Homo sapi

c	34	212.8	98.5	56835	2	AC025369	AC025369 Homo sapi
	35	195.2	90.4	3018	10	AF288666	AF288666 Mus muscu
	36	193.6	89.6	4139	10	BC062979	BC062979 Mus muscu
	37	193.6	89.6	4702	10	BC059238	BC059238 Mus muscu
	38	193.6	89.6	169529	10	AC124466	AC124466 Mus muscu
c	39	193.6	89.6	170386	2	AC124181	AC124181 Mus muscu
	40	193.6	89.6	184366	10	AC121783	AC121783 Mus muscu
	41	193.6	89.6	237974	2	AC094771	AC094771 Rattus no
c	42	193.6	89.6	253924	2	AC126707	AC126707 Rattus no
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	44	55	25.5	1853	6	AX879717	AX879717 Sequence
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ALIGNMENTS

RESULT 1

AX026743

LOCUS AX026743 216 bp DNA linear PAT 16-SEP-2000
 DEFINITION Sequence 3 from Patent WO0031252.
 ACCESSION AX026743
 VERSION AX026743.1 GI:10187888
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Klostermann,A. and Behl,C.
 TITLE Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal
 development and regeneration mechanisms during apoptosis, and its
 use as a potential drug target
 JOURNAL Patent: WO 0031252-A 3 02-JUN-2000;
 KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL
 CHRISTIAN (DE)
 FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 216;
 Best Local Similarity 100.0%; Pred. No. 1.2e-41;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
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Db      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
QY      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
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RESULT 2

AX876167

LOCUS AX876167 2123 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 11072 from Patent EP1074617.
ACCESSION AX876167
VERSION AX876167.1 GI:40030903
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 11072 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES Location/Qualifiers
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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1611
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 QY 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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 Db 1612 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1647

RESULT 3

BD155987

LOCUS BD155987 2123 bp DNA linear PAT 17-JAN-2003
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD155987
 VERSION BD155987.1 GI:27861745
 KEYWORDS JP 2002191363-A/10830.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2123)
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002191363-A 10830 09-JUL-2002;
 HELIX RESEARCH INSTITUTE
 COMMENT OS Homo sapiens (human)
 PN JP 2002191363-A/10830
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI SAITO,
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUJI OTSUKI
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10,
 PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
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 FT CDS (127)..(1647).
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Query Match 100.0%; Score 216; DB 6; Length 2123;

Best Local Similarity 100.0%; Pred. No. 9.2e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1611

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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RESULT 4

AK027439

LOCUS AK027439 2123 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FLJ14533 fis, clone NT2RM2000407, moderately similar to *Mus musculus* semaphorin VIa mRNA.
ACCESSION AK027439
VERSION AK027439.1 GI:14042113
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2123)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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Query Match 100.0%; Score 216; DB 9; Length 2123;
Best Local Similarity 100.0%; Pred. No. 9.2e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db	1612 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1647

RESULT 5

BD127394

LOCUS	BD127394	2227 bp	DNA	linear	PAT 18-SEP-2002
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.				
ACCESSION	BD127394				
VERSION	BD127394.1 GI:23222339				
KEYWORDS	JP 2002017375-A/2825.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

REFERENCE 1 (bases 1 to 2227)
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
 Koga,H.
 TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002017375-A 2825 22-JAN-2002;
 HELIX RESEARCH INSTITUTE
 COMMENT OS Homo sapiens (human)
 PN JP 2002017375-A/2825
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253172
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
 PI ISHII,
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
 SHINICHI KOJIMA,
 PI TETSUJI OTSUKI, HISASHI KOGA
 PC
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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 Primer for synthesizing full-length cDNA and use thereof FH Key
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 Db 1706 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1741

RESULT 6
AK074975
LOCUS AK074975 2227 bp mRNA linear PRI 03-SEP-2002
DEFINITION Homo sapiens cDNA FLJ90494 fis, clone NT2RP3003614.
ACCESSION AK074975
VERSION AK074975.1 GI:22760768

KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
 Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
 Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
 Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
 Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
 Ninomiya,K.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2227)
 AUTHORS Isogai,T. and Otsuki,T.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction:
 Institute of Medical Science, University of Tokyo, Laboratory of
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
 sequencing and clone selection: Helix Research Institute (supported
 by Japan Key Technology Center etc.).
 FEATURES Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RP3003614"
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 /note="cloning vector: pME18SFL3~mRNA from NT2 neuronal
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 induction"
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 /note="unnamed protein product"
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 ORIGIN

Query Match

100.0%; Score 216; DB 9; Length 2227;

Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 GGGCTGAACCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
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Db 1646 GGGCTGAACCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1705

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Db 1706 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1741

RESULT 7

AX879422

LOCUS AX879422 2293 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 14327 from Patent EP1074617.
ACCESSION AX879422
VERSION AX879422.1 GI:40034158
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 14327 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES Location/Qualifiers
source 1. .2293
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS 138. .1826
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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2293;
Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
Db 1668 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 1727

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC 180
Db 1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC 1787

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 1788 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1823

RESULT 8

BD157826

LOCUS BD157826 2293 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD157826
VERSION BD157826.1 GI:27863584
KEYWORDS JP 2002191363-A/12669.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2293)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 12669 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/12669
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (138)..(1823).
FEATURES Location/Qualifiers
source 1..2293

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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2293;
Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db 1608 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1667
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QY 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
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QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
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Db 1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1787
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QY 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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Db 1788 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1823

RESULT 9

AK027471

LOCUS AK027471 2293 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FLJ14565 fis, clone NT2RM4000233, highly similar to *Mus musculus* semaphorin VIa mRNA.
ACCESSION AK027471
VERSION AK027471.1 GI:14042170
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2293)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction,

5' - & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES Location/Qualifiers
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 /note="cloning vector: pUC19FL3-mRNA from uninduced NT2 neuronal precursor cells."
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ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 2293;
Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
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Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 120
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Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
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Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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Db 1788 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1823

RESULT 10

AX882662

LOCUS AX882662 2306 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 17567 from Patent EP1074617.

ACCESSION AX882662
 VERSION AX882662.1 GI:40037563
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primers for synthesising full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 17567 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES Location/Qualifiers
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 MKPNDACT"
 ORIGIN
 Query Match 100.0%; Score 216; DB 6; Length 2306;
 Best Local Similarity 100.0%; Pred. No. 9.1e-42;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 CCGCCGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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 Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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 Db 1795 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1830

Db 1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830

RESULT 12
AK027654
LOCUS AK027654 2306 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FLJ14748 fis, clone NT2RP3002869, highly similar to Mus musculus semaphorin VIa mRNA.
ACCESSION AK027654
VERSION AK027654.1 GI:14042491
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2306)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
FEATURES Location/Qualifiers
source 1. .2306
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP3002869"
/cell_line="NT2"
/cell_type="teratocarcinoma"
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/note="cloning vector: pME18SFL3~mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."
CDS 109. .1833
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MKPNDACT"

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 2306;
Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
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Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC 180
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Db 1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC 1794

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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Db 1795 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1830

RESULT 13

AX882248

LOCUS AX882248 3041 bp DNA linear PAT 17-DEC-2003

DEFINITION Sequence 17153 from Patent EP1074617.

ACCESSION AX882248

VERSION AX882248.1 GI:40037065

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primers for synthesising full-length cDNA and their use

JOURNAL Patent: EP 1074617-A 17153 07-FEB-2001;
Research Association for Biotechnology (JP)

FEATURES Location/Qualifiers

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RLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESRGGMWDWK
HLLDSPDSTDPLGAVSSHNNHQDKKGVIRESYLKGDQLVPVTLLAIAVI LAFVMGAVF
SGITVYVCVDHRRKDVAVQRKEKELTHSRRGSMSSVTKLSGLFGDTQS KDPKPEAIL
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PSFAPLSTS MKPNDACT"

ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 3041;
Best Local Similarity 100.0%; Pred. No. 8.8e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	60
Db	1966	CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	2025
Qy	61	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG	120
Db	2026	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG	2085
Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC	180
Db	2086	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC	2145
Qy	181	CTTCCACATCCATGAAGCCAATGATGCGTGTACA	216
Db	2146	CTTCCACATCCATGAAGCCAATGATGCGTGTACA	2181

RESULT 14

BD159617

LOCUS BD159617 3041 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD159617
VERSION BD159617.1 GI:27865375
KEYWORDS JP 2002191363-A/14460.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3041)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 14460 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/14460

PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI Saito,
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUJI OTSUKI
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10,
 PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
 Location/Qualifiers
 FT CDS (85). .(2181).
FEATURES
 source Location/Qualifiers
 1. .3041
 /organism="Homo sapiens"
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ORIGIN

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Query Match      100.0%;  Score 216;  DB 6;  Length 3041;
Best Local Similarity 100.0%;  Pred. No. 8.8e-42;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db      1966 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCTACAACACTCACTGACAAGGTCG 120
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||  

Db      2026 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCTACAACACTCACTGACAAGGTCG 2085

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||  

Db      2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 2145

Qy      181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
        ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  

Db      2146 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 2181
  
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RESULT 15

AK027501

LOCUS AK027501 3041 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FLJ14595 fis, clone NT2RM4002194, highly similar
 to *Mus musculus* semaphorin VIa mRNA.
ACCESSION AK027501
VERSION AK027501.1 GI:14042222
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
 Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,

Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
 Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
 Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
 Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3041)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction,
 5'- & 3'-end one pass sequencing and clone selection: Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.
FEATURES Location/Qualifiers
 source 1. .3041
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RM4002194"
 /cell_line="NT2"
 /cell_type="teratocarcinoma"
 /clone_lib="NT2RM4"
 /note="cloning vector: pUC19FL3-mRNA from uninduced NT2
 neuronal precursor cells."
 CDS 85. .2184
 /note="unnamed protein product"
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 NHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVDNSEKCSYDGVEDKRIMGMQ
 LDRASSSLYVAFSTCVIKVPLGRERHGKCKTCIASRDPYCGWIKEGGACSHLSPNS
 RLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSQDSTAQEYESRGGMILDWK
 HLLDSPDSTDPLGAVSSHNDKKGVIRESYLYKGHDQLPVTLLAIAVILA
 FVMGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRGSMSSVTKLSGLFGDTQS
 KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTA
 LPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPV
 IPTDLPLRASP
 SHIPS
 VSVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKT
 IKEHLSSSKSPN
 HGVL
 ENLDSL
 PPKV
 QREASLG
 PPPGASLSQ
 TGLSKRLEMHHSSSYGV
 DVYKRSYPT
 NSL
 TRSHQATT
 LKRNN
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 STSM
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 DACT"

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 3041;
 Best Local Similarity 100.0%; Pred. No. 8.8e-42;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db	1966 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTG 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2026 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTG 2085

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 2145

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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Db 2146 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 2181

Search completed: March 26, 2004, 03:40:52

Job time : 859.974 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 19:45:25 ; Search time 86.4914 Seconds
(without alignments)
10609.274 Million cell updates/sec

Title: US-09-856-681A-3

Perfect score: 216

Sequence: 1 ccggccgcccgcggcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002s:
7: geneseqn2003as:
8: geneseqn2003bs:
9: geneseqn2003cs:
10: geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					Description
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1	216	100.0	216	3	AAD01234	Aad01234 DNA encod
2	216	100.0	1472	3	AAC98050	Aac98050 Human col
3	216	100.0	2123	4	AAH13995	Aah13995 Human cDN
4	216	100.0	2227	4	AAK94365	Aak94365 Human ful
5	216	100.0	2262	6	ABK34739	Abk34739 Human cDN
6	216	100.0	2293	4	AAH15834	Aah15834 Human cDN
7	216	100.0	2306	4	AAH17861	Aah17861 Human cDN

8	216	100.0	2592	5	AAS68253	Aas68253 DNA encod	
9	216	100.0	3039	5	AAS68807	Aas68807 DNA encod	
10	216	100.0	3039	5	AAS89721	Aas89721 DNA encod	
11	216	100.0	3041	4	AAH17625	Aah17625 Human cDN	
12	216	100.0	3333	3	AAA93618	Aaa93618 Human sem	
13	216	100.0	3333	8	ADA23282	Ada23282 cDNA enco	
14	216	100.0	3498	3	AAA93617	Aaa93617 Human sem	
15	216	100.0	3498	8	ADA23280	Ada23280 cDNA enco	
16	216	100.0	3550	2	AAV44295	Aav44295 Human sec	
17	216	100.0	3550	5	AAF98469	Aaf98469 Human cDN	
18	216	100.0	3862	3	AAD01233	Aad01233 Human sem	
19	216	100.0	4250	8	ADA23361	Ada23361 cDNA enco	
20	216	100.0	4280	7	ABX71103	Abx71103 Novel hum	
21	216	100.0	4564	8	ACH03994	Ach03994 Human cDN	
22	216	100.0	6060	4	AAH18729	Aah18729 Human cDN	
c	23	168	77.8	460	8	ACH16587	Ach16587 Human adu
	24	55	25.5	1853	4	AAH15994	Aah15994 Human cDN
	25	55	25.5	2581	4	AAH16063	Aah16063 Human cDN
	26	55	25.5	3196	6	ABS64382	Abs64382 Human sem
	27	55	25.5	3205	6	ABS64380	Abs64380 Human sem
	28	55	25.5	3364	6	ABS64384	Abs64384 Human sem
	29	55	25.5	3694	4	AAH42597	Aah42597 Nucleotid
	30	55	25.5	4234	6	ABA00055	Aba00055 CADHP-2 c
	31	55	25.5	6645	7	ABX34714	Abx34714 Human mdd
	32	55	25.5	6767	4	AAL04256	Aal04256 Human rep
	33	55	25.5	6773	4	AAL04255	Aal04255 Human rep
	34	53.4	24.7	662	4	AAL00809	Aal00809 Human rep
c	35	42.8	19.8	575	4	AAH10827	Aah10827 Human cDN
	36	36.8	17.0	670	5	AAC90703	Aac90703 Human sec
c	37	35.4	16.4	1971	2	AAV58278	Aav58278 Fluoresce
	38	35.2	16.3	936	7	ABT21228	Abt21228 Aspergill
	39	35.2	16.3	936	7	ABT19408	Abt19408 Aspergill
	40	35.2	16.3	1015	7	ABT18814	Abt18814 Aspergill
	41	35.2	16.3	1015	7	ABT20630	Abt20630 Aspergill
	42	35.2	16.3	3015	7	ABT18220	Abt18220 Aspergill
	43	35.2	16.3	3015	7	ABT20034	Abt20034 Aspergill
c	44	35.2	16.3	13987	2	AAT80415	Aat80415 Hybrid sr
c	45	35.2	16.3	43280	2	AAT80413	Aat80413 Tylactone

ALIGNMENTS

RESULT 1
 AAD01234
 ID AAD01234 standard; DNA; 216 BP.
 XX
 AC AAD01234;
 XX
 DT 04-OCT-2000 (first entry)
 XX
 DE DNA encoding binding domain of human semaphorin 6A-1.
 XX
 KW Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;
 KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;
 KW gene therapy; diagnostic agent; therapeutic agent; differentiation;
 KW cytoskeletal stabilisation; plasticity; ds.

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .216
FT /*tag= a
FT /product= "Binding domain of semaphorin 6A-1"
FT /note= "The binding domain shows homology to Zyxin
FT protein and selectively binds to members of Ena/VASP
FT protein family, especially Evl; the CDS does not include
FT stop codon"
FT /partial
XX
PN WO200031252-A1.
XX
PD 02-JUN-2000.
XX
PF 26-NOV-1999; 99WO-EP009215.
XX
PR 26-NOV-1998; 98EP-00122441.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Behl C, Klostermann A;
XX
DR WPI; 2000-400065/34.
DR P-PSDB; AAY71461.
XX
PT Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT therapeutic agent, for modulating immune system, in gene therapy or for
PT effecting differentiation, cytoskeletal stabilization and/or plasticity.
XX
PS Claim 2; Page 21; 53pp; English.
XX
CC The present sequence is a DNA encoding binding domain of transmembranous
CC human semaphorin 6A-1 ((HSA)SEMA6A-1) which is involved in neuronal
CC development and regeneration mechanisms during apoptosis. The binding
CC domain shows homology to Zyxin protein and selectively binds to members
CC of Ena/VASP protein family, especially Evl. (HSA)SEMA6A-1 is a member of
CC protein family displaying secreted or transmembrane-based repulsive
CC guidance cues critically involved in neuronal development. Expression of
CC (HSA)SEMA6A-1 is highest in embryonic brain and kidney and moderate in
CC lung. The present sequence is useful as diagnostic and therapeutic
CC agents, for modulating the immune system, in gene therapy, for effecting
CC differentiation, cytoskeletal stabilisation and plasticity
XX
SQ Sequence 216 BP; 45 A; 85 C; 51 G; 35 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 3; Length 216;
Best Local Similarity 100.0%; Pred. No. 2.7e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

QY 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120

|||
Db 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 120
|||
Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
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Db 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
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Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
|||
Db 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216

RESULT 2

AAC98050

ID AAC98050 standard; cDNA; 1472 BP.

XX

AC AAC98050;

XX

DT 09-MAR-2001 (first entry)

XX

DE Human colon cancer antigen nucleotide sequence SEQ ID NO:60.

XX

KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200055351-A1.

XX

PD 21-SEP-2000.

XX

PF 08-MAR-2000; 2000WO-US005883.

XX

PR 12-MAR-1999; 99US-0124270P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX

DR WPI; 2000-587534/55.

DR P-PSDB; AAB53293.

XX

PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.

XX

PS Claim 1; Page 510-511; 2104pp; English.

XX

CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,

CC vulnerable, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention

XX

SQ Sequence 1472 BP; 437 A; 431 C; 299 G; 301 T; 0 U; 4 Other;

Query Match 100.0%; Score 216; DB 3; Length 1472;
Best Local Similarity 100.0%; Pred. No. 4.3e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
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Db 372 CCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 431

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACACTCACTGACAAGGTCG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 432 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACACTCACTGACAAGGTCG 491

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 551

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 552 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 587

RESULT 3

AAH13995

ID AAH13995 standard; cDNA; 2123 BP.

XX

AC AAH13995;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:11072.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

Db 1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1611
Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1612 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1647

RESULT 4

AAK94365

ID AAK94365 standard; cDNA; 2227 BP.

XX

AC AAK94365;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human full-length cDNA, SEQ ID NO: 3087.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI; 2001-524255/58.

DR P-PSDB; AAM93444.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.

XX

PS Claim 8; SEQ ID NO 3087; 1380pp + Sequence Listing; English.

XX

CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a full length human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in CD-ROM format directly
CC from EPO

XX

SQ Sequence 2227 BP; 567 A; 700 C; 560 G; 400 T; 0 U; 0 Other;
Query Match 100.0%; Score 216; DB 4; Length 2227;
Best Local Similarity 100.0%; Pred. No. 4.7e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCGCAGAGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1526 CCGCCGCCCCGCCCGCAGAGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1585

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1586 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 1645

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1705

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||||||||||||||||||||||||||||||||
Db 1706 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1741

RESULT 5
ABK34739
ID ABK34739 standard; cDNA; 2262 BP.
XX
AC ABK34739;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human cDNA for novel secreted protein, SEQ ID 508.
XX
KW Human; ss; gene; secreted protein; immune deficiency; viral infection;
KW bacterial infection; fungal infection; autoimmune disorder; burn;
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
KW lymphoid cell deficiency.
XX
OS Homo sapiens.
XX
PN WO200177290-A2.
XX
PD 18-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US010295.
XX
PR 06-APR-2000; 2000US-0194941P.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
XX

DR WPI; 2002-179323/23.

XX

PT Six hundred and twenty five polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.

XX

PS Claim 1; Page 272; 339pp; English.

XX

CC The invention relates to 625 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins, their complements and sequences that hybridise to them. Also
CC included are a vector comprising the polynucleotide, a host cell
CC transformed with the vector, the proteins encoded by the polynucleotides,
CC antibodies that bind to the proteins and identification of modulators of
CC the proteins or the expression of the polynucleotide. The polynucleotides
CC can be used as probes for the identification and isolation of full length
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used
CC as nutritional supplements. The protein is useful in the treatment of
CC various immune deficiencies and disorders such as viral infections,
CC bacterial infections, fungal infections, autoimmune disorders (e.g.
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and
CC tumours. They are also useful for tissue regeneration, for wound healing
CC and in the treatment of burns, incisions and ulcers. The proteins are
CC also useful for regulating haematopoiesis, for treating myeloid or
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
CC sequences encoding a secreted protein

XX

SQ Sequence 2262 BP; 604 A; 695 C; 522 G; 441 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 6; Length 2262;
Best Local Similarity 100.0%; Pred. No. 4.7e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 1184 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1243

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 1244 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 1303

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 1304 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1363

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
Db 1364 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1399

RESULT 6

AAH15834

ID AAH15834 standard; cDNA; 2293 BP.

XX
AC AAH15834;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14327.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
PS Claim 8; SEQ ID NO 14327; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent

CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX

SQ Sequence 2293 BP; 579 A; 713 C; 581 G; 420 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 4; Length 2293;
Best Local Similarity 100.0%; Pred. No. 4.8e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1608 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1667

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1668 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 1727

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 1787

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1788 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 1823

RESULT 7
AAH17861
ID AAH17861 standard; cDNA; 2306 BP.
XX
AC AAH17861;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:17567.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX

DR WPI; 2001-318749/34.

xx

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

xx

PS Claim 8; SEQ ID NO 17567; 2537pp + Sequence Listing; English.

xx

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

xx

SQ Sequence 2306 BP; 579 A; 739 C; 577 G; 411 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 4; Length 2306;
 Best Local Similarity 100.0%; Pred. No. 4.8e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGGCCCCCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGGCCATCTGGC 60
|||||

Db 1615 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1674

QY 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTAACGCCTACAACTCAGTACAAGGTCG 120
DQ 1675 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTAACGCCTACAACTCAGTACAAGGTCG 120

QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180

Pb 1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAAACCATCTTTGCTCCC 1794

Qy 181 CTTTCCACATCCATGAAGGCCAATGATGCGTGTACA 216

|||||

Db 1795 CTTTCCACATCCATGAAGGCCAATGATGCGTGTACA 1830

RESULT 8

AAS68253

ID AAS68253 standard; cDNA; 2592 BP.
XX
AC AAS68253;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #4057.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG04066.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 4057; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences

XX
SQ Sequence 2592 BP; 655 A; 754 C; 659 G; 524 T; 0 U; 0 Other;
Query Match 100.0%; Score 216; DB 5; Length 2592;
Best Local Similarity 100.0%; Pred. No. 4.9e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2374 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2433
QY 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2434 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 2493
QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2494 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 2553
QY 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2554 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 2589

RESULT 9
AAS68807
ID AAS68807 standard; cDNA; 3039 BP.
XX
AC AAS68807;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #4611.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG04620.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

PS Claim 1; SEQ ID NO 4611; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 5; Length 3039;
Best Local Similarity 100.0%; Pred. No. 5.1e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2821 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 2880

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2881 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 2940

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2941 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3000

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3001 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3036

RESULT 10
AAS89721
ID AAS89721 standard; cDNA; 3039 BP.
XX
AC AAS89721;
XX
DT 13-FEB-2002 (first entry)

XX
DE DNA encoding novel human diagnostic protein #25525.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG25534.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 25525; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 5; Length 3039;
Best Local Similarity 100.0%; Pred. No. 5.1e-52;

Matches	216;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	60						
Db	2821	CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	2880						
Qy	61	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTG	120						
Db	2881	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTG	2940						
Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC	180						
Db	2941	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC	3000						
Qy	181	CTTTCCACATCCATGAAGCCAATGATGCGTGTACA	216						
Db	3001	CTTTCCACATCCATGAAGCCAATGATGCGTGTACA	3036						

RESULT 11

AAH17625

ID AAH17625 standard; cDNA; 3041 BP.

XX

AC AAH17625;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:17153.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

PS Claim 8; SEQ ID NO 17153; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 3041 BP; 804 A; 886 C; 714 G; 637 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 4; Length 3041;
Best Local Similarity 100.0%; Pred. No. 5.1e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1966 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 2026 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 2085

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 2145

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 2146 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2181

RESULT 12

AAA93618

ID AAA93618 standard; DNA; 3333 BP.

XX

AC AAA93618;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant SECX 2864933-2 DNA.

XX
KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200053742-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006280.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 08-MAR-2000; 2000US-0520781P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;
XX
DR WPI; 2000-594318/56.
DR P-PSDB; AAB23031.
XX
PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.
XX
PS Claim 3; Fig 3; 15lpp; English.
XX
CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
CC the invention are either secreted or membrane-associated proteins and act
CC as regulator of cellular proliferation and differentiation. SECX proteins
CC or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of a
CC SECX protein with other cellular proteins may be useful to modulate the
CC activity of a partner protein, cellular proliferation, cellular
CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in a
CC biological sample, and in forensic biology. SECX primers or probes are
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or
CC prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders

CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders
XX

SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 0 U; 1 Other;

Query Match 100.0%; Score 216; DB 3; Length 3333;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2925 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

QY 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2985 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 3044

QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3104

QY 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3105 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3140

RESULT 13
ADA23282
ID ADA23282 standard; cDNA; 3333 BP.
XX
AC ADA23282;
XX
DT 20-NOV-2003 (first entry)
XX
DE cDNA encoding human SECX polypeptide, SEC3 #1.
XX
KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX

PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelle WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23283.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Fig 3; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.
XX
SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 0 U; 1 Other;

Query Match 100.0%; Score 216; DB 8; Length 3333;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2925 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2985 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 3044

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3104

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3105 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3140

RESULT 14

AAA93617

ID AAA93617 standard; DNA; 3498 BP.

XX

AC AAA93617;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ds.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR P-PSDB; AAB23030.

XX

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 3; Fig 2; 15lpp; English.

XX

CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
CC the invention are either secreted or membrane-associated proteins and act
CC as regulator of cellular proliferation and differentiation. SECX proteins
CC or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of a
CC SECX protein with other cellular proteins may be useful to modulate the
CC activity of a partner protein, cellular proliferation, cellular

CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in a
CC biological sample, and in forensic biology. SECX primers or probes are
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or
CC prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

Query Match 100.0%; Score 216; DB 3; Length 3498;
Best Local Similarity 100.0%; Pred. No. 5.3e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3090 CCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3149

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTGCG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3150 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTGCG 3209

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3210 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3269

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
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Db 3270 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3305

RESULT 15

ADA23280

ID ADA23280 standard; cDNA; 3498 BP.

XX

AC ADA23280;

XX

DT 20-NOV-2003 (first entry)

XX

DE cDNA encoding human SECX polypeptide, SEC2.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelele WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23281.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Fig 2; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.
XX
SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

Query Match 100.0%; Score 216; DB 8; Length 3498;
Best Local Similarity 100.0%; Pred. No. 5.3e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
Db 3090 CCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 3149
Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120

Db 3150 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 3209
Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
|||
Db 3210 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3269
Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
|||
Db 3270 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3305

Search completed: March 26, 2004, 00:01:21
Job time : 87.4914 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:24:56 ; Search time 15.7969 Seconds
(without alignments)
7588.151 Million cell updates/sec

Title: US-09-856-681A-3

Perfect score: 216

Sequence: 1 ccggccgcccgcggcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
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	1	55	25.5	3261	4	US-09-653-274-5 Sequence 5, Appli
	2	55	25.5	3694	4	US-09-653-274-3 Sequence 3, Appli
c	3	35.4	16.4	1971	2	US-08-818-253-7 Sequence 7, Appli
c	4	35.4	16.4	1971	3	US-08-818-252-7 Sequence 7, Appli
c	5	35.2	16.3	13987	2	US-08-804-227C-13 Sequence 13, Appli
c	6	35.2	16.3	43280	2	US-08-804-227C-1 Sequence 1, Appli
c	7	34.4	15.9	4403765	3	US-09-103-840A-2 Sequence 2, Appli
c	8	34.4	15.9	4411529	3	US-09-103-840A-1 Sequence 1, Appli
c	9	33.8	15.6	846	4	US-09-252-991A-8905 Sequence 8905, Ap
10	33.8	15.6	1026	4	US-09-252-991A-1737 Sequence 1737, Ap	
11	33.8	15.6	2667	4	US-09-252-991A-9254 Sequence 9254, Ap	

c	12	33.8	15.6	3228	4	US-09-252-991A-1816	Sequence 1816, Ap
c	13	33.8	15.6	3546	4	US-09-252-991A-2143	Sequence 2143, Ap
c	14	33.2	15.4	630	4	US-09-252-991A-7012	Sequence 7012, Ap
	15	33.2	15.4	1548	4	US-09-252-991A-7061	Sequence 7061, Ap
	16	33.2	15.4	1581	4	US-09-252-991A-7117	Sequence 7117, Ap
	17	33	15.3	1536	3	US-08-993-359-29	Sequence 29, Appl
	18	33	15.3	1536	4	US-09-482-558A-29	Sequence 29, Appl
	19	32	14.8	1153	2	US-08-869-793-5	Sequence 5, Appl
	20	32	14.8	1162	4	US-09-620-312D-982	Sequence 982, App
	21	31.8	14.7	1119	4	US-09-170-496D-65	Sequence 65, Appl
	22	31.8	14.7	1119	4	US-09-170-496D-199	Sequence 199, App
	23	31.8	14.7	1679	1	US-08-202-056-6	Sequence 6, Appl
	24	31.8	14.7	1679	1	US-08-076-093A-5	Sequence 5, Appl
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	33	31.8	14.7	2818	3	US-08-982-493-7	Sequence 7, Appl
	34	31.8	14.7	2818	3	US-08-628-655-1	Sequence 1, Appl
c	35	31.6	14.6	882	4	US-09-252-991A-1751	Sequence 1751, Ap
	36	31.6	14.6	1449	4	US-09-252-991A-1976	Sequence 1976, Ap
	37	31.2	14.4	1320	3	US-09-221-654-1	Sequence 1, Appl
	38	31.2	14.4	1320	3	US-08-989-358A-1	Sequence 1, Appl
	39	31.2	14.4	1593	3	US-08-993-359-23	Sequence 23, Appl
	40	31.2	14.4	1593	4	US-09-482-558A-23	Sequence 23, Appl
c	41	31.2	14.4	1932	4	US-09-215-418-3	Sequence 3, Appl
	42	30.6	14.2	432	4	US-09-593-887-7	Sequence 7, Appl
	43	30.6	14.2	720	4	US-09-839-650-1	Sequence 1, Appl
c	44	30.6	14.2	4833	4	US-09-513-783A-21	Sequence 21, Appl
c	45	30.4	14.1	77536	4	US-09-410-551B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-653-274-5

```
; Sequence 5, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
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; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-653-274-5

Query Match 25.5%; Score 55; DB 4; Length 3261;
Best Local Similarity 64.6%; Pred. No. 8.1e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 74 TCTCGAGGCAGCCCAGCCTCAACGCTACAACTCACTGACAAGGTGGGGCTGAAGCGTA 133
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Qy 134 CGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCTTCCACATCCA 193
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Db 3173 CGCCGTCTTAAACCTGACGTGCCACCAAGCCTCCTTGTTCCTCAAACCCATCTG 3232

Qy 194 TGAAGCC 200
| | ||
Db 3233 TCAGACC 3239

RESULT 2

US-09-653-274-3
; Sequence 3, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (434)..(3694)
US-09-653-274-3

Query Match 25.5%; Score 55; DB 4; Length 3694;

Best Local Similarity 64.6%; Pred. No. 8.3e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 74 TCTCGAGGCAGCCCAGCCTCAACGCCTACAACACTCACTGACAAGGTGGGGCTGAAGCGTA 133
||||| ||| |||| | ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3546 TCTCCAGACAGAGCAGCTACACCAGTAATGGCACTCTTCTTAGGACGGGACTAAAGAGGA 3605

Qy 134 CGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCTTCCACATCCA 193
||||| ||| |||| | | ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3606 CGCCGTCCCTTAAACCTGACGTGCCACCAAGCCTTCCTTGTTCCTCAAACCCATCTG 3665

Qy 194 TGAAGCC 200
| | | |
Db 3666 TCAGACC 3672

RESULT 3

US-08-818-253-7/c

; Sequence 7, Application US/08818253

; Patent No. 5998204

; GENERAL INFORMATION:

; APPLICANT: Tsien, Roger Y.

; APPLICANT: Miyawaki, Atsushi

; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR

; TITLE OF INVENTION: DETECTION OF ANALYTES

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/818,253

; FILING DATE: 14-MAR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Ph.D., Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07257/043001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1971 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1968
US-08-818-253-7

Query Match 16.4%; Score 35.4; DB 2; Length 1971;
Best Local Similarity 61.3%; Pred. No. 0.34;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 CGCCGTCCAGCTCGACCAGGATGGGCACCACCCGGTGAACAGCTCCTGCCCTTGCTCA 53

Qy 62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCA 94
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 CGTCGGCGGCAGCAGCAGGCCAGCAGCAGCA 20

RESULT 4

US-08-818-252-7/c

; Sequence 7, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1968)

US-08-818-252-7

Query Match 16.4%; Score 35.4; DB 3; Length 1971;
Best Local Similarity 61.3%; Pred. No. 0.34;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 CGCCGTCCAGCTCGACCAGGATGGGCACCACCCGGTGAACAGCTCCTGCCCTTGCTCA 53

Qy 62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCA 94
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 CGTCGGCGGCAGCAGCAGGCCAGCAGCAGCA 20

RESULT 5

US-08-804-227C-13/c

; Sequence 13, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rosteck, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..13987

US-08-804-227C-13

Query Match 16.3%; Score 35.2; DB 2; Length 13987;
Best Local Similarity 48.5%; Pred. No. 0.67;
Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
|| || || . || | || | || || || | || || || || || || || || || || || ||
Db 1346 CGGCGAGCGGCCTGCTGCAGGCCGCTGTCCGCCCGCCCCGAGCACGGCGCCAGTGCAG 1287

Qy 62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCGG 121
|| || || | || | | | | | | | | | || || || || || || || || || || || || ||
Db 1286 CCGCCTCGACGGGGTCGCCGGCCGGTGCAGCTCGACGTAGCGGACGG 1227

Qy 122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCC 181
|| | || || || || | | | || | || || || || || || || || || || || || || || ||

Db 1226 CGCCGGTGCTGACGCCGCCGCCGGTAGGCCTGGCGCAGCACAGCTCCTGCGCCTCCC 1167
Qy 182 TTTCCACATCCATGAAGCCC 201
|| | ||| |||
Db 1166 GGTGGGAGTGTTGAGGCTC 1147

RESULT 6

US-08-804-227C-1/c

; Sequence 1, Application US/08804227C

; Patent No. 5876991

; GENERAL INFORMATION:

; APPLICANT: DeHoff, Bradley S.

; APPLICANT: Kuhstoss, Stuart A.

; APPLICANT: Rosteck, Paul R., Jr.

; APPLICANT: Sutton, Kimberly L.

; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: THOMAS G. PLANT 1501

; STREET: LILLY CORPORATE CENTER

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: ASCII(DOS) Text only

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/804,227C

; FILING DATE: February 21, 1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Plant, Thomas, G.

; REGISTRATION NUMBER: 35,784

; REFERENCE/DOCKET NUMBER: X-8231

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-2459

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43280 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 816..14234

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 14351..19945

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 20010..31199

; FEATURE:

```

;      NAME/KEY:  CDS
;      LOCATION:  31232..36067
; FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  36249..41774
US-08-804-227C-1

Query Match          16.3%;  Score 35.2;  DB 2;  Length 43280;
Best Local Similarity 48.5%;  Pred. No. 0.91;
Matches   97;  Conservative    0;  Mismatches  103;  Indels     0;  Gaps     0;

Qy      2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
        ||||| ||| | ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      1896 CGGGAGCGGGCGTGCCTGCGGCCGCTGTCGCCGGCGCCCGAGCACGGCGCCAGTGCAG 1837

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTGG 121
        ||||| ||| | ||| | | | | | | | | | | | | | | | | | | | | | | |
Db      1836 CCGCCTCGACGGGGTCGCCGGCGCCGGTAGGCCTGGCGCAGCACAGCTCAGCTAGCGGACGG 1777

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCC 181
        ||| | ||| ||| | | | | | | | | | | | | | | | | | | | | | | |
Db      1776 CGCCGGTGCTGACGCCGCCCGCCGGTAGGCCTGGCGCAGCACAGCTCCTGCCCTCCC 1717

Qy      182 TTTCCACATCCATGAAGCCC 201
        ||| | ||| | | |
Db      1716 GGTGGGAGTGGTGAGGCTC 1697

```

RESULT 7

US-09-103-840A-2/c

```

; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

```

```

Query Match          15.9%;  Score 34.4;  DB 3;  Length 4403765;
Best Local Similarity 57.4%;  Pred. No. 5.3;
Matches   62;  Conservative    0;  Mismatches  46;  Indels     0;  Gaps     0;

```

```

Qy      22 GTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGG 81
       | | | | ||| || | | ||||| | | | | | | | | | | | | | | | | | | | |
Db      745995 GGGTATTCCCTCGTAGAGGGCCAGCTCGTTGGCTACCCGGCCGGCGCGATCAGCTGGCGG
745936

Qy      82 CAGCCCAGCCTCAACGCCTACAACACTCACTGACAAGGTGGGGCTGAAG 129
       | | | | ||| || | | ||||| | | | | | | | | | | | | | | | |
Db      745935 CCGTCCTGCACCAGCGACGACAACGCCCGCCACGCTCGGGTCGACG 745888

```

RESULT 8

US-09-103-840A-1/c

; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match 15.9%; Score 34.4; DB 3; Length 4411529;
Best Local Similarity 57.4%; Pred. No. 5.3;
Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```

Qy      22 GTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGG 81
       | | | | ||| || | | ||||| | | | | | | | | | | | | | | | | | | |
Db      744035 GGGTATTCCCTCGTAGAGGGCCAGCTCGTTGGCTACCCGGCCGGCGCGATCAGCTGGCGG
743976

Qy      82 CAGCCCAGCCTCAACGCCTACAACACTCACTGACAAGGTGGGGCTGAAG 129
       | | | | ||| || | | ||||| | | | | | | | | | | | | | | |
Db      743975 CCGTCCTGCACCAGCGACGACAACGCCCGCCACGCTCGGGTCGACG 743928

```

RESULT 9

US-09-252-991A-8905/c

; Sequence 8905, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8905
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8905

Query Match 15.6%; Score 33.8; DB 4; Length 846;
Best Local Similarity 49.2%; Pred. No. 0.79;
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
|| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 343 CGTGGCAGCGCGAGCACATCTTCTGCGCCATCGCCTTGCCGCCAGGTCGGCGGGCG 284

Qy 62 AGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTGG 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 283 CGTCCGGGCCGGCACGGCGGCCAGCGGCAGGGAAAGCAGGGCCGAGAGGCAGCCGG 224

Qy 122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCC 181
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 CCAGCCAGCGTTACGCTCAGTCATGCTGCCAGGGCCCCGCAGCCAGCCGTGGATGTCG 164

Qy 182 T 182
|
Db 163 T 163

RESULT 10

US-09-252-991A-1737
; Sequence 1737, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1737
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1737

Query Match 15.6%; Score 33.8; DB 4; Length 1026;
 Best Local Similarity 54.4%; Pred. No. 0.84;
 Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTCGG 121
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      271 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 330
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCC 181
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      331 GAAGGAAGAGCGCGGCAACAAGGGCGCCGCCCCTGACCACCTCATCAGCCTGGCGGCCG 390
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      182 TTTCC 186
        || ||
Db      391 TTACC 395
  
```

RESULT 11

US-09-252-991A-9254

; Sequence 9254, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 9254
 ; LENGTH: 2667
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9254

Query Match 15.6%; Score 33.8; DB 4; Length 2667;
 Best Local Similarity 49.2%; Pred. No. 1.1;
 Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

```

Qy      2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGCC 61
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38 CGTGGCAGCGCGAGCACATCTCTGCGCCATGCCCTGCGCGCAGGTCGGCGGGCG 97
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTCGG 121
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      98 CGTCCGGGCCGGCACGGCGGGCAGCGGCAGGGAAAGCAGGGCGAGAGGCAGCCGG 157
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCC 181
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      158 CCAGCCAGCGTTACGCTCAGTCATGCTGCCAGGGCCCCCGCAGCCAGCCGTGGATGTCG 217
  
```


; PRIORITY APPLICATION NUMBER: US 60/074,788
; PRIORITY FILING DATE: 1998-02-18
; PRIORITY APPLICATION NUMBER: US 60/094,190
; PRIORITY FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2143
; LENGTH: 3546
; TYPE: DNA
; ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-2143

[View Details](#)

```

Query Match           15.6%; Score 33.8; DB 4; Length 3546;
Best Local Similarity 54.4%; Pred. No. 1.2;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy      62 AGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCCTACAACTCACTGACAAGGTCGG 121
        ||||||| | ||||| ||| | ||||| ||| | ||||| ||| ||| | | ||||| |
Db      3064 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 3005

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCCC 181
        | | ||| | | ||| | | ||||| | ||| | | ||| | | | | | | | | |
Db      3004 GAAGGAAGAGCGCGCAACAAGGGCGCCGCCCTGACCACCTTCATCAGCCTGGCCGGCCG 2945

Qy      182 TTTCC 186
        ||| |
Db      2944 TTACC 2940

```

RESULT 14

US-09-252-991A-7012/c

; Sequence 7012, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

PSEUDOMONAS

• TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: 03
PRIOR FILING DATE: 1998-03-18

; PRIOR FILING DATE: 1998-02-18
; PCT/US98/03000
; PCT/US98/03000

; PRIORITY APPLICATION NUMBER: US 60/094,190
; FILING DATE: 1999-07-27

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7012

; LENGTH: 630

; TYPE: DNA

; ORGANISM: P

US-09-252-991A

Query Match

Best Local Similarity 53.0%; Pred. No. 1.1;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Db 203 CCTGCCGCGCATCGAGGTGGATGCCGCATGCCGCCGTCCGGCCGGCTGGCTGGCG 144
Qy 67 GTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTGGCTG 126
| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 143 CATCTATCGTGGAGCCCGCCATGAGCATGGCTTCCAGCCGTTCCAAGGAGGCCGAC 84
Qy 127 AAGCGTACGCCCTC 140
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 83 AGGCAGTCGCCCTC 70

RESULT 15

US-09-252-991A-7061

; Sequence 7061, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7061
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7061

Query Match 15.4%; Score 33.2; DB 4; Length 1548;
Best Local Similarity 53.0%; Pred. No. 1.4;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 7 CCCGCCCGCAGAGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGCCAGGCC 66
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 532 CCTGCCGCGCATCGAGGTGGATGCCGCATGCCGCCGTCCGGCCGGCTGGCTGGCG 591
Qy 67 GTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTGGCTG 126
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 592 CATCTATCGTGGAGCCCGCCATGAGCATGGCTTCCAGCCGTTCCAAGGAGGCCGAC 651
Qy 127 AAGCGTACGCCCTC 140
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 652 AGGCAGTCGCCCTC 665

Search completed: March 26, 2004, 03:46:11

Job time : 23.7969 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:27:11 ; Search time 76.6346 Seconds
(without alignments)
10493.560 Million cell updates/sec

Title: US-09-856-681A-3

Perfect score: 216

Sequence: 1 ccggccgccccccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC

Gapext 1.0 , Gapext 1.0

Searched: 2458946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query				
No.	Score	Match	Length	DB	ID
					Description

c	1	216	100.0	569	14	US-10-029-386-11004	Sequence 11004, A
c	2	216	100.0	1199	14	US-10-029-386-24706	Sequence 24706, A
	3	216	100.0	1472	9	US-09-925-299-60	Sequence 60, Appl
	4	216	100.0	1472	10	US-09-925-299-60	Sequence 60, Appl
	5	216	100.0	2944	12	US-10-403-676-29	Sequence 29, Appl
	6	216	100.0	2944	15	US-10-449-548-29	Sequence 29, Appl
	7	216	100.0	2995	12	US-10-403-676-19	Sequence 19, Appl
	8	216	100.0	2995	15	US-10-449-548-19	Sequence 19, Appl
	9	216	100.0	3055	12	US-10-403-676-27	Sequence 27, Appl
	10	216	100.0	3055	15	US-10-449-548-27	Sequence 27, Appl
	11	216	100.0	3106	12	US-10-403-676-17	Sequence 17, Appl
	12	216	100.0	3106	15	US-10-449-548-17	Sequence 17, Appl
	13	216	100.0	3165	12	US-10-403-676-47	Sequence 47, Appl
	14	216	100.0	3165	15	US-10-449-548-47	Sequence 47, Appl
	15	216	100.0	3333	10	US-09-991-053-5	Sequence 5, Appli
	16	216	100.0	3333	10	US-09-957-187-5	Sequence 5, Appli
	17	216	100.0	3498	10	US-09-991-053-3	Sequence 3, Appli
	18	216	100.0	3498	10	US-09-957-187-3	Sequence 3, Appli
	19	216	100.0	3498	12	US-10-403-676-31	Sequence 31, Appl
	20	216	100.0	3498	15	US-10-449-548-31	Sequence 31, Appl
	21	216	100.0	3983	12	US-10-403-676-45	Sequence 45, Appl
	22	216	100.0	3983	15	US-10-449-548-45	Sequence 45, Appl
	23	216	100.0	4250	10	US-09-957-187-84	Sequence 84, Appl
	24	216	100.0	4250	12	US-10-403-676-13	Sequence 13, Appl
	25	216	100.0	4250	14	US-10-393-892-30	Sequence 30, Appl
	26	216	100.0	4250	14	US-10-394-382-30	Sequence 30, Appl
	27	216	100.0	4250	15	US-10-449-548-13	Sequence 13, Appl
	28	216	100.0	4280	15	US-10-120-988-330	Sequence 330, App
c	29	168	77.8	460	10	US-09-918-995-3799	Sequence 3799, Ap
	30	55	25.5	3196	12	US-10-016-248-15	Sequence 15, Appl
	31	55	25.5	3205	12	US-10-016-248-11	Sequence 11, Appl
	32	55	25.5	3364	12	US-10-016-248-19	Sequence 19, Appl
	33	55	25.5	6767	10	US-09-764-891-6944	Sequence 6944, Ap
	34	55	25.5	6773	10	US-09-764-891-6943	Sequence 6943, Ap
	35	53.4	24.7	662	10	US-09-764-891-810	Sequence 810, App
c	36	37.4	17.3	765	15	US-10-027-632-166826	Sequence 166826,
c	37	35.4	16.4	1971	9	US-09-554-000-7	Sequence 7, Appli
	38	35.2	16.3	936	14	US-10-128-714-2578	Sequence 2578, Ap
	39	35.2	16.3	936	14	US-10-128-714-7578	Sequence 7578, Ap
	40	35.2	16.3	1015	14	US-10-128-714-1578	Sequence 1578, Ap
	41	35.2	16.3	1015	14	US-10-128-714-6578	Sequence 6578, Ap
	42	35.2	16.3	3015	14	US-10-128-714-578	Sequence 578, App
	43	35.2	16.3	3015	14	US-10-128-714-5578	Sequence 5578, Ap
	44	35	16.2	1473	15	US-10-369-493-41703	Sequence 41703, A
c	45	34.4	15.9	31263	12	US-10-282-122A-25447	Sequence 25447, A

ALIGNMENTS

RESULT 1

US-10-029-386-11004/c

; Sequence 11004, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11004
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008524.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: gi14728537, EVALU 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE898612.1, EVALU 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q62523, EVALU 1.20e-01
US-10-029-386-11004

Query Match 100.0%; Score 216; DB 14; Length 569;
Best Local Similarity 100.0%; Pred. No. 6.7e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 552 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 493

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 492 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 433

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 432 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 373

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 372 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 337

RESULT 2
US-10-029-386-24706/c
; Sequence 24706, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24706
; LENGTH: 1199
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008524.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: gi14728537, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: O35464, EVALUE 1.00e-125
; OTHER INFORMATION: EST_HUMAN HIT: AW954605.1, EVALUE 0.00e+00
US-10-029-386-24706

Query Match 100.0%; Score 216; DB 14; Length 1199;
Best Local Similarity 100.0%; Pred. No. 7.2e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 219 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 160

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 159 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 100

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 99 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 40

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 39 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 4

RESULT 3

US-09-925-299-60
; Sequence 60, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-299-60

Query Match 100.0%; Score 216; DB 9; Length 1472;
Best Local Similarity 100.0%; Pred. No. 7.4e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCAGAGGGTGGACTCCATCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db 372 CCGCCGCCGCAGAGGGTGGACTCCATCAGGTGCACAGCTCCCAGCCATCTGGC 431

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
|||
Db 432 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 491

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
|||
Db 492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 551

Qy 181 CTTCACATCCATGAAGCCAATGATGCGTGTACA 216
|||
Db 552 CTTCACATCCATGAAGCCAATGATGCGTGTACA 587

RESULT 4

US-09-925-299-60

; Sequence 60, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-299-60

Query Match 100.0%; Score 216; DB 10; Length 1472;
Best Local Similarity 100.0%; Pred. No. 7.4e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 372 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 431

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
Db 432 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 491

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 551

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 552 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 587

RESULT 5

US-10-403-676-29

; Sequence 29, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 29
; LENGTH: 2944
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2944)
US-10-403-676-29

Query Match 100.0%; Score 216; DB 12; Length 2944;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 2720 CCGCCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2779

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 2780 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 2839

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 2840 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 2899

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 2900 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 2935

RESULT 6

US-10-449-548-29

; Sequence 29, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 29
; LENGTH: 2944
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2944)

US-10-449-548-29

Query Match 100.0%; Score 216; DB 15; Length 2944;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

Db 2720 CCGCCGCCGCCGCAGAGGGTGGACTCCATCAGGTGACAGCTCCCAGCCATCTGGC 2779
Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCAGTGACAAGGTCG 120
Db 2780 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCAGTGACAAGGTCG 2839
Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 2840 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 2899
Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 2900 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 2935

RESULT 7

US-10-403-676-19

; Sequence 19, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 19
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2995)

US-10-403-676-19

Query Match 100.0%; Score 216; DB 12; Length 2995;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|||
Db 2771 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2830

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
|||
Db 2831 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 2890

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
|||
Db 2891 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 2950

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
|||
Db 2951 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 2986

RESULT 8

US-10-449-548-19
; Sequence 19, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 19
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2995)

US-10-449-548-19

Query Match 100.0%; Score 216; DB 15; Length 2995;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
Db 2771 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 2830

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCAGTACAAGGTCG 120
Db 2831 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACTCAGTACAAGGTCG 2890

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTGCTCCC 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2891 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTGCTCCC 2950

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2951 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 2986

RESULT 9

US-10-403-676-27

; Sequence 27, Application US/10403676
; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 27
; LENGTH: 3055
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3055)
US-10-403-676-27

Query Match 100.0%; Score 216; DB 12; Length 3055;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
Db 2831 CCGCCGCCGCCGCAGAGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 2890

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 120
Db 2891 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACTCACTGACAAGGTCG 2950

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 2951 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3010

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 3011 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3046

RESULT 10

US-10-449-548-27

; Sequence 27, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 27
; LENGTH: 3055
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3055)
US-10-449-548-27

Query Match 100.0%; Score 216; DB 15; Length 3055;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	60
Db	2831	CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	2890
Qy	61	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG	120
Db	2891	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG	2950
Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC	180
Db	2951	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCC	3010
Qy	181	CTTCCACATCCATGAAGCCAATGATGCGTGTACA	216
Db	3011	CTTCCACATCCATGAAGCCAATGATGCGTGTACA	3046

RESULT 11
US-10-403-676-17
; Sequence 17, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojaia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23

; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 17
; LENGTH: 3106
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3106)
US-10-403-676-17

Query Match 100.0%; Score 216; DB 12; Length 3106;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 2882 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2941

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
Db 2942 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 3001

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 3002 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3061

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 3062 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3097

RESULT 12
US-10-449-548-17
; Sequence 17, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 17
; LENGTH: 3106
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3106)
US-10-449-548-17

Query Match 100.0%; Score 216; DB 15; Length 3106;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
Db 2882 CCGCCGCCGCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 2941

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 2942 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 3001

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 3002 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3061

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 3062 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3097

RESULT 13
US-10-403-676-47
; Sequence 47, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 47
; LENGTH: 3165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3153)
US-10-403-676-47

Query Match 100.0%; Score 216; DB 12; Length 3165;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCAGAGGGTGGACTCCATCAGGTGCACAGCTCCCAGCCATCTGGC 60
Db 2938 CCGCCGCCGCAGAGGGTGGACTCCATCAGGTGCACAGCTCCCAGCCATCTGGC 2997

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
Db 2998 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 3057

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
Db 3058 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3117

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
Db 3118 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3153

RESULT 14

US-10-449-548-47

; Sequence 47, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798

; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 47
; LENGTH: 3165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3153)
US-10-449-548-47

Query Match 100.0%; Score 216; DB 15; Length 3165;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCGCCGCCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 2938 CCGCCGCCGCCGCCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2997

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 120
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 2998 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTAACGCCTACAACACTCACTGACAAGGTG 3057

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 3058 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3117

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 3118 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3153

RESULT 15
US-09-991-053-5
; Sequence 5, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
; TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 15966-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: USSN 60/123,667

; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(2865)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2882)
; OTHER INFORMATION: an n may be any one of a or t or g or c

US-09-991-053-5

Query Match 100.0%; Score 216; DB 10; Length 3333;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGGCGCAGAGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|||
Db 2925 CCGCCGCCCCGGCGCAGAGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 120
|||
Db 2985 CAGGCCGTGACTGTCTCGAGGCAGGCCAGCCTAACGCCTACAACACTCACTGACAAGGTCG 3044

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 180
|||
Db 3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTGCTCCC 3104

Qy 181 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 216
|||
Db 3105 CTTTCCACATCCATGAAGCCAATGATGCGTGTACA 3140

Search completed: March 26, 2004, 04:05:56
Job time : 78.6346 secs